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Joseph F. Hicklin

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EXAMINER

SKOWRONEK, KARLHEINZ R

ART UNIT

PAPER NUMBER

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PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

| | | | |
|------------------------------|---|---------------------------------------|--|
| Office Action Summary | Application No. 10/783,552 | Applicant(s) HICKLIN ET AL. | |
| | Examiner KARLHEINZ R. SKOWRONEK | Art Unit 1631 | |

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 19 November 2009.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-39 is/are pending in the application.
- 4a) Of the above claim(s) 6,7,12,13,18,19,24,25,30,31 and 36 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-5,8-11,14-17,20-23,26-29,32-35 and 37-39 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|---|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413) |
| 2) <input type="checkbox"/> Notice of Draftperson's Patent Drawing Review (PTO-948) | Paper No(s)/Mail Date. _____ |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08) | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| Paper No(s)/Mail Date _____ | 6) <input type="checkbox"/> Other: _____ |

DETAILED ACTION

Claim Status

Claims 1-39 are pending.

Claims 6-7, 12-13, 18-19, 24-25, 30-31, and 36 are withdrawn as being directed to a non-elected invention, the election having been made on 19 March 2007.

Claims 1-5, 8-11, 14-17, 20-23, 26-29, 32-35, and 37-39 have been examined.

Claims 1-5, 8-11, 14-17, 20-23, 26-29, 32-35, and 37-39 are rejected.

Priority

This application was filed on 20 February 2004 and makes no claims to the benefit of any earlier filed applications.

Claim Objections

Claims 8, 14, 26, and 32 are objected to because of the following informalities:

The claims recite the phrase "if the amount the data gathered from the experiment differs from the generated dynamic behavior is greater that the predetermined amount". The phrase contains various typographical errors. The phrase is interpreted to be "if the difference between the gathered data and the generated dynamic behavior is greater than the predetermined amount". The phrase occurs in claim 8 at line 14-16, in claim 14 at lines 18-19, in claim 26 at lines 14-16, and in claim 32 at lines 19-20. Appropriate correction is required.

Claim Rejections - 35 USC § 103

Art Unit: 1631

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

The factual inquiries set forth in *Graham v. John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

The following rejection is necessitated by amendment.

Claims 1-5 and 20-23 are rejected under 35 U.S.C. 103(a) as being unpatentable over Sauro et al., in view of Kurata et al., in view of Funhashi et al. (Biosilico, Vol. 1 No. 3, p. 159-162, 2003 November) and in view of Allen et al (US PG PUB 2002/0068269)

The claims are directed to a system, computer-implemented method, and computer program product for improved modeling of a biological system, a biological system being a plurality of chemical reactions, comprising a modeling component with a graphical user interface to generate a model; a simulation engine accepting the model and generating a dynamic behavior for the biologic system; and an analysis environment that interfaces with data acquisition hardware that gathers experimental data and using the gather data to generate or modify the model.

Sauro et al. show a system, computer-implemented method, and computer program product for improved modeling of a biological system, a biological system being a plurality of chemical reactions, comprising a modeling component with a graphical user interface (GUI) to generate a model; a simulation engine accepting the model and generating a dynamic behavior for the biologic system; and an analysis environment to display the dynamic behavior (figure 11). The system implemented by Sauro et al. integrates several stand-alone programs in a way such that the inputs and outputs of each program can be exchanged with the other programs, i.e. the programs are SBW-compliant or enabled. Sauro et al. shows the integration of the programs of JDesigner, Jarnac, and SBW Meta-tool (p. 365, Applications). In figure 11 of Sauro et al, the elements of modeling component having a GUI providing means for accepting user input via a tool palette to generate a block diagram of a plurality of related chemical

Art Unit: 1631

reactions that make a biological system. The figure also depicts an analysis environment displaying the dynamic behavior of the biological system, and a simulation engine. The system of Sauro et al. integrates several different programs as components and facilitates the intercommunication of the programs to provide a dynamic, high performance framework for modeling biological systems and reaction pathways (p. 355). Figure 12 shows that in addition to depicting the model graphically, the model is also displayed as a table. Figure 12 shows screen shot of JDesigner interfaced with METATOOL. Sauro et al. shows JDesigner acts as a model editor from which users can initiate simulation and METATOOL analysis (p. 368). In the lower left portion of figure 12, the tabular view of METATOOL displays the modes, sets of enzymes working together at steady state to construct a plausible subpathways, of the reactions representative of the model displayed in graphical format in the center of figure 12. Thus, Sauro et al. shows the adaptation of the tabular view to receive user commands and input to construct the model. Sauro et al. show that the dynamic behavior of the system is modeled using a stochastic computational model (p 355 and 364). Sauro et al. also shows that models are entered in the form of a script stored in SBML level 1. Sauro et al. shows the JARNAC tool is a script based simulation tool using models stored in SBML level 1 (p. 366). The SBML script is another tabular form of a model.

Sauro et al. does not explicitly show the display of one or more reactions in tabular form.

Kurata et al. shows a computational system for the modeling of biochemical reaction networks. Kurata et al. shows that a portion of the model is displayed in tabular

form and the tables have at least one chemical reaction (figure 3). Kurata et al. shows the benefit of the GUI is it allows one to draw and describe a large-scale map of molecular networks (p. 4076, col. 1). Kurata et al suggests the CADLIVE system not only constructs a large-scale map of complicated signal transduction pathways based on the information provided by molecular biology, but also has the capability to map the heterogeneous experimental data derived from DNA microarrays and proteomics studies on a biochemical network of interest (4084, col. 1).

Sauro et al. in view of Kurata et al. do not show a reaction table with a plurality of reactions and a species table that depicts at least one initial condition and amount of material.

Funhashi et al. shows in figure 1 table of reactions (bottom left) with a plurality of reaction and a table of species (bottom right) with at least an initial condition and an amount of a starting material. The relevant portion of figure 1 is included here for clarity.

| Type | ID | Name | Reagent | Product | Matrix |
|------------------|-----|-------|---------|---------|--------|
| STATE_TRANSITION | r1 | Hydro | Hydro | g21 | g22 |
| STATE_TRANSITION | g2 | Hydro | Hydro | g11 | g12 |
| STATE_TRANSITION | g7 | Hydro | Hydro | g4 | g7 |
| STATE_TRANSITION | g8 | Hydro | Hydro | g22 | g4 |
| STATE_TRANSITION | r13 | Hydro | Hydro | g23 | g8 |
| STATE_TRANSITION | r12 | Hydro | Hydro | g24 | g8 |

| Type | ID | Name | Comp | PK | Units | No | CR |
|---------|-----|----------|------|------|-------|----|----|
| PROTEIN | g3 | CyclinB | g3 | 0.0 | mol | 31 | 34 |
| PROTEIN | g4 | WAP | g3 | 0.01 | mol | 31 | 34 |
| PROTEIN | g5 | WAPase X | g3 | 0.01 | mol | 31 | 34 |
| PROTEIN | g7 | CAR | g3 | 0.01 | mol | 31 | 34 |
| PROTEIN | g13 | Hydro | g3 | 0.0 | mol | 31 | 34 |
| PROTEIN | g11 | Hydro | g3 | 0.0 | mol | 31 | 34 |
| PROTEIN | g12 | Hydro | g3 | 0.01 | mol | 31 | 34 |

Funhashi et al. shows the standardized model description enhances the portability of the models between software tools (p. 160, col. 1).

Allen et al is drawn to a method and system for simulating biochemical pathways. Allen et al shows that shows an analysis environment that interfaces with data acquisition hardware that gathers experimental data [0048]. Allen et al shows using the gather data to generate or modify the model [0049-0050]. Allen et al shows the

Art Unit: 1631

configuration of an analysis engine interfaced with data acquisition hardware advantageously provides output information regarding the role and physiological importance of new gene products or gene products with altered expression [0050].

It would have been obvious to one of ordinary skill in the art at the time of invention to modify the biological simulation system of Sauro et al. with the display of Kurata et al. because Kurata et al. shows that a benefit of the display is it allows one to draw and describe a large scale map of molecular networks. It would have been further obvious to one of skill in the art at the time of invention to modify the biological simulation of Sauro et al. in view of Kurata et al. with the tabular views of Funhashi et al. because Funhashi et al. shows standardized model description enhances the portability of the models between software tools. It would have been further obvious to one of ordinary skill in the art at the time of invention to modify the biological simulation system of Sauro et al. with the display of Kurata et al. and the editing of reaction and species via a tabular view of Funhashi et al. because all the claimed elements were known, in the prior art, and one skilled in the art could have combined the elements as claimed by known methods with no change in their respective functions, and the combination would have yielded nothing more than predictable results to one of ordinary skill in the art at the time of the invention. It would have been further obvious to one of ordinary skill in the art at the time of invention to modify the biological simulation system of Sauro et al. using the display of Kurata et al. and the editing of reaction and species via a tabular view of Funhashi et al. with the interfacing of data acquisition hardware of Allen et al. because Allen et al. shows the configuration of an analysis engine interfaced with data

Art Unit: 1631

acquisition hardware advantageously provides output information regarding the role and physiological importance of new gene products or gene products with altered expression.

Response to Arguments

Applicant's arguments filed 19 November 2009 have been fully considered but they are not persuasive. Applicant argues that Sauro et al., in view of Kurata et al., and in view of Funhashi et al. fails to show and an analysis environment that interfaces with data acquisition hardware that gathers experimental data and using the gather data to generate or modify the model. This is not persuasive because Allen et al. shows and an analysis environment that interfaces with data acquisition hardware that gathers experimental data and using the gather data to generate or modify the model. In addition, Kurata et al suggests the CADLIVE system not only constructs a large-scale map of complicated signal transduction pathways based on the information provided by molecular biology, but also has the capability to map the heterogeneous experimental data derived from DNA microarrays and proteomics studies on a biochemical network of interest (4084, col. 1).

The following rejection is necessitated by amendment.

Claims 8-11, 14-17, 26-29, and 32-35 are rejected under 35 U.S.C. 103(a) as being unpatentable over Sauro et al., in view of Kurata et al., in view of Funhashi et al. (Biosilico, Vol. 1 No. 3, p. 159-162, 2003 November) and in view of Schilling et al (US PG PUB 2003/0233218).

Art Unit: 1631

The claims are directed to a system, computer-implemented method, and computer program product for improved modeling of a biological system, a biological system being a plurality of chemical reactions, comprising a modeling component with a graphical user interface to generate a model; a simulation engine accepting the model and generating a dynamic behavior for the biologic system; and providing an indication that the difference between the gathered data and the dynamic behavior is greater a threshold level.

Sauro et al. show a system, computer-implemented method, and computer program product for improved modeling of a biological system, a biological system being a plurality of chemical reactions, comprising a modeling component with a graphical user interface (GUI) to generate a model; a simulation engine accepting the model and generating a dynamic behavior for the biologic system; and an analysis environment to display the dynamic behavior (figure 11). The system implemented by Sauro et al. integrates several stand-alone programs in a way such that the inputs and outputs of each program can be exchanged with the other programs, i.e. the programs are SBW-compliant or enabled. Sauro et al. shows the integration of the programs of JDesigner, Jarnac, and SBW Meta-tool (p. 365, Applications). In figure 11 of Sauro et al, the elements of modeling component having a GUI providing means for accepting user input via a tool palette to generate a block diagram of a plurality of related chemical reactions that make a biological system. The figure also depicts an analysis environment displaying the dynamic behavior of the biological system, and a simulation engine. The system of Sauro et al. integrates several different programs as components

Art Unit: 1631

and facilitates the intercommunication of the programs to provide a dynamic, high performance framework for modeling biological systems and reaction pathways (p. 355). Figure 12 shows that in addition to depicting the model graphically, the model is also displayed as a table. Figure 12 shows screen shot of JDesigner interfaced with METATOOL. Sauro et al. shows JDesigner acts as a model editor from which users can initiate simulation and METATOOL analysis (p. 368). In the lower left portion of figure 12, the tabular view of METATOOL displays the modes, sets of enzymes working together at steady state to construct a plausible subpathways, of the reactions representative of the model displayed in graphical format in the center of figure 12. Thus, Sauro et al. shows the adaptation of the tabular view to receive user commands and input to construct the model. Sauro et al. show that the dynamic behavior of the system is modeled using a stochastic computational model (p 355 and 364). Sauro et al. also shows that models are entered in the form of a script stored in SBML level 1. Sauro et al. shows the JARNAC tool is a script based simulation tool using models stored in SBML level 1 (p. 366). The SBML script is another tabular form of a model.

Sauro et al. does not explicitly show the display of one or more reactions in tabular form.

Kurata et al. shows a computational system for the modeling of biochemical reaction networks. Kurata et al. shows that a portion of the model is displayed in tabular form and the tables have at least one chemical reaction (figure 3). Kurata et al. shows the benefit of the GUI is it allows one to draw and describe a large-scale map of molecular networks (p. 4076, col. 1).

Sauro et al. in view of Kurata et al. do not show a reaction table with a plurality of reactions and a species table that depicts at least one initial condition and amount of material.

Funhashi et al. shows in figure 1 table of reactions (bottom left) with a plurality of reaction and a table of species (bottom right) with at least an initial condition and an amount of a starting material. The relevant portion of figure 1 is included here for clarity.

| id | name | rate | initial | final | species | amount | method |
|---------------------|--------------------|------|---------|-------|---------|--------|--------|
| STATE_TRANSITION_01 | State 1 to State 2 | 0.1 | 0.1 | 0.1 | State 1 | 0.1 | 0.1 |
| STATE_TRANSITION_02 | State 2 to State 1 | 0.1 | 0.1 | 0.1 | State 2 | 0.1 | 0.1 |
| STATE_TRANSITION_03 | State 1 to State 3 | 0.1 | 0.1 | 0.1 | State 1 | 0.1 | 0.1 |
| STATE_TRANSITION_04 | State 2 to State 3 | 0.1 | 0.1 | 0.1 | State 2 | 0.1 | 0.1 |
| STATE_TRANSITION_05 | State 3 to State 1 | 0.1 | 0.1 | 0.1 | State 3 | 0.1 | 0.1 |
| STATE_TRANSITION_06 | State 3 to State 2 | 0.1 | 0.1 | 0.1 | State 3 | 0.1 | 0.1 |
| STATE_TRANSITION_07 | State 1 to State 4 | 0.1 | 0.1 | 0.1 | State 1 | 0.1 | 0.1 |
| STATE_TRANSITION_08 | State 2 to State 4 | 0.1 | 0.1 | 0.1 | State 2 | 0.1 | 0.1 |
| STATE_TRANSITION_09 | State 3 to State 4 | 0.1 | 0.1 | 0.1 | State 3 | 0.1 | 0.1 |
| STATE_TRANSITION_10 | State 4 to State 1 | 0.1 | 0.1 | 0.1 | State 4 | 0.1 | 0.1 |
| STATE_TRANSITION_11 | State 4 to State 2 | 0.1 | 0.1 | 0.1 | State 4 | 0.1 | 0.1 |
| STATE_TRANSITION_12 | State 4 to State 3 | 0.1 | 0.1 | 0.1 | State 4 | 0.1 | 0.1 |

| id | name | comp | init | units | init | conc | val |
|------------|------------|------|------|-------|------|------|-----|
| SPECIES_01 | Species 1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| SPECIES_02 | Species 2 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| SPECIES_03 | Species 3 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| SPECIES_04 | Species 4 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| SPECIES_05 | Species 5 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| SPECIES_06 | Species 6 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| SPECIES_07 | Species 7 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| SPECIES_08 | Species 8 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| SPECIES_09 | Species 9 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| SPECIES_10 | Species 10 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| SPECIES_11 | Species 11 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| SPECIES_12 | Species 12 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |

Funhashi et al. shows the standardized model description enhances the portability of the models between software tools (p. 160, col. 1).

Schilling et al shows a system and method for modeling a biological network. Schilling shows that experimental data is used to determine values of confidence [0131-0132]. Schilling et al shows that threshold level is set by a user which is used to compare gathered data to the model [0135]. Schilling et al. shows that rating levels are determined, reading on an indicator [0135]. Schilling et al. shows that the use of confidence levels or values of confidence enhance model specificity and provide the advantage of maintaining quality control and accountability for the content of the model [0127].

It would have been obvious to one of ordinary skill in the art at the time of invention to modify the biological simulation system of Sauro et al. with the display of Kurata et al. because Kurata et al. shows that a benefit of the display is it allows one to

Art Unit: 1631

draw and describe a large scale map of molecular networks. It would have been further obvious to one of skill in the art at the time of invention to modify the biological simulation of Sauro et al. in view of Kurata et al. with the tabular views of Funhashi et al. because Funhashi et al. shows standardized model description enhances the portability of the models between software tools. It would have been further obvious to one of ordinary skill in the art at the time of invention to modify the biological simulation system of Sauro et al. with the display of Kurata et al. and the editing of reaction and species via a tabular view of Funhashi et al. because all the claimed elements were known, in the prior art, and one skilled in the art could have combined the elements as claimed by known methods with no change in their respective functions, and the combination would have yielded nothing more than predictable results to one of ordinary skill in the art at the time of the invention. It would have been further obvious to one of ordinary skill in the art at the time of invention to modify the biological simulation system of Sauro et al., the display of Kurata et al. and the editing of reaction and species via a tabular view of Funhashi et al. with the confidence levels and threshold values of Schilling et al. because Schilling et al. shows that the use of confidence levels or values of confidence enhance model specificity and provide the advantage of maintaining quality control and accountability for the content of the model.

Response to Arguments

Applicant's arguments filed 06 July 2009 have been fully considered but they are not persuasive. Applicant argues that Sauro et al., in view of Kurata et al., and in view of Funhashi et al. fails to show a step of providing an indication that the difference

Art Unit: 1631

between the gathered data and the dynamic behavior is greater a threshold level. The argument is not persuasive. Schilling shows that experimental data is used to determine values of confidence [0131-0132]. Schilling et al shows that threshold level is set by a user which is used to compare gathered data to the model [0135]. Schilling et al. shows that rating levels are determined, reading on an indicator [0135]. Thus, Schilling et al. shows a step of providing an indication that the difference between the gathered data and the dynamic behavior is greater a threshold level.

The following rejection is necessitated by amendment.

Claim 37 is rejected under 35 U.S.C. 103(a) as being unpatentable over Sauro et al. and in view of Kurata et al. in view of Funhashi et al. and in view of Allen et al. as applied to claims 1-5 and 20-23 above, and further in view of Shannon et al. (Genome Research, Vol. 13, p. 2498-2504, 2003) and in view of Biospice (Presentation of Biospice, DARPA BioComp, May 2002).

Claim 37 is directed to embodiment in which user annotations are displayed in a column in a table and in a location close to an element in the graphical view.

Sauro et al. and in view of Kurata et al. in view of Funhashi et al. and in view of Allen et al. as applied to claims 1-5 and 20-23 above above show a computational system for modeling chemical reactions.

Sauro et al. and in view of Kurata et al. in view of Funhashi et al. and in view of Allen et al. does not explicitly show user annotations are displayed in a column view and in a location close to an element in the graphical view.

Art Unit: 1631

Shannon et al. shows a system for simulating biochemical reactions and interactions. Shannon et al. shows that data is integrated with the graph model using attributes (p. 2499, col. 2). Shannon et al. shows that attribute values may assume any type (e.g., text strings, discrete or continuous numbers, URLs, or lists) and are either loaded from a data repository or generated dynamically within a session reading on user annotations (p. 2499, col. 2). Shannon shows in figure 1a table with annotations in a column view. Shannon et al. shows that it is possible to have many levels of annotation all active and on display at the same time, each as a different attribute on the nodes or edges of interest (p. 2500, col. 1-2). Shannon et al. shows that annotations are transferred on to the nodes and edges (p. 2500, col. 1). Shannon et al. shows that by visually superimposing molecular states on the interaction pathways hypothesized to regulate those states, attribute-to-visual mappings directly connect observed data to an underlying model (p. 2500, col. 2).

Biospice shows annotations are localized close to elements in the graphical view (p. 32).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to modify the system for modeling biochemical reactions of Sauro et al. and in view of Sauro et al. and in view of Kurata et al. in view of Funhashi et al. and in view of Allen et al. as applied to claims 1-5 and 20-23 above with annotations in a column and localized close to elements in the graphical view as shown by Shannon et al. and Biospice because all the claimed elements were known, in the prior art, and one skilled in the art could have combined the elements as claimed by known methods with

Art Unit: 1631

no change in their respective functions, and the combination would have yielded nothing more than predictable results to one of ordinary skill in the art at the time of the invention. It would have been obvious to one of ordinary skill in the art at the time the invention was made to modify the system for modeling biochemical reactions of Sauro et al. and in view of Kurata et al. in view of Funhashi et al. and in view of Allen et al. as applied to claims 1-5 and 20-23 above with annotations in a column and localized close to elements in the graphical view as shown by Shannon et al. and Biospice because Shannon et al. shows by visually superimposing molecular states on the interaction pathways hypothesized to regulate those states, attribute-to-visual mappings directly connect observed data to an underlying model.

The following rejection is necessitated by amendment.

Claims 38-39 are rejected under 35 U.S.C. 103(a) as being unpatentable over Sauro et al. and in view of Kurata et al. in view of Funhashi et al. and in view of Schilling et al. as applied to claims 8-11, 14-17, 26-29, and 32-35 above, and further in view of Shannon et al. (Genome Research, Vol. 13, p. 2498-2504, 2003) and in view of Biospice (Presentation of Biospice, DARPA BioComp, May 2002).

Claims 38-39 are directed to embodiment in which user annotations are displayed in a column in a table and in a location close to an element in the graphical view.

Sauro et al. and in view of Kurata et al. in view of Funhashi et al. and in view of Schilling et al. as applied to claims 8-11, 14-17, 26-29, and 32-35 above above show a computational system for modeling chemical reactions.

Sauro et al. and in view of Kurata et al. in view of Funhashi et al. and in view of Schilling et al. does not explicitly show user annotations are displayed in a column view and in a location close to an element in the graphical view.

Shannon et al. shows a system for simulating biochemical reactions and interactions. Shannon et al. shows that data is integrated with the graph model using attributes (p. 2499, col. 2). Shannon et al. shows that attribute values may assume any type (e.g., text strings, discrete or continuous numbers, URLs, or lists) and are either loaded from a data repository or generated dynamically within a session reading on user annotations (p. 2499, col. 2). Shannon shows in figure 1a table with annotations in a column view. Shannon et al. shows that it is possible to have many levels of annotation all active and on display at the same time, each as a different attribute on the nodes or edges of interest (p. 2500, col. 1-2). Shannon et al. shows that annotations are transferred on to the nodes and edges (p. 2500, col. 1). Shannon et al. shows that by visually superimposing molecular states on the interaction pathways hypothesized to regulate those states, attribute-to-visual mappings directly connect observed data to an underlying model (p. 2500, col. 2).

Biospice shows annotations are localized close to elements in the graphical view (p. 32).

Art Unit: 1631

It would have been obvious to one of ordinary skill in the art at the time the invention was made to modify the system for modeling biochemical reactions of Sauro et al. and in view of Sauro et al. and in view of Kurata et al. in view of Funhashi et al. and in view of Schilling et al. as applied to claims 8-11, 14-17, 26-29, and 32-35 above with annotations in a column and localized close to elements in the graphical view as shown by Shannon et al. and Biospice because all the claimed elements were known, in the prior art, and one skilled in the art could have combined the elements as claimed by known methods with no change in their respective functions, and the combination would have yielded nothing more than predictable results to one of ordinary skill in the art at the time of the invention. It would have been obvious to one of ordinary skill in the art at the time the invention was made to modify the system for modeling biochemical reactions of Sauro et al. and in view of Kurata et al. in view of Funhashi et al. and in view of Schilling et al. as applied to claims 8-11, 14-17, 26-29, and 32-35 above with annotations in a column and localized close to elements in the graphical view as shown by Shannon et al. and Biospice because Shannon et al. shows by visually superimposing molecular states on the interaction pathways hypothesized to regulate those states, attribute-to-visual mappings directly connect observed data to an underlying model.

Response to Arguments

Applicant's arguments filed 19 November 2009 have been fully considered but they are not persuasive. Applicant argues that Sauro et al. and in view of Kurata et al. and in view of Funhashi et al. as applied to claims 1-5, 8-11, 14-17, 20-23, 26-29, and

Art Unit: 1631

32-35 above, and further in view of Shannon et al. and in view of Biospice fails to show a step of providing an indication that the difference between the gathered data and the dynamic behavior is greater a threshold level. The argument is not persuasive. This is not persuasive because Schilling et al. shows a step of providing an indication that the difference between the gathered data and the dynamic behavior is greater a threshold level.

Conclusion

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to KARLHEINZ R. SKOWRONEK whose telephone

Art Unit: 1631

number is (571)272-9047. The examiner can normally be reached on 8:00am-5:00pm Monday-Friday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran can be reached on (571) 272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/KARLHEINZ R SKOWRONEK/
Examiner, Art Unit 1631

16 March 2010